```
CLASSIFICATION: HEAVY CONSTANT CHAINS (cont'd)
             97) MOPC173: MOUSE IGG2A
     97) MOPC173: MOUSE IGG2A
98) CEPC101: MOUSE IGG2A
99) IGA*CL: MOUSE IGA
100) IGA*CL*: MOUSE IGA
101) MOPC47A: MOUSE IGA
102) MOPC47A: MOUSE IGA
103) MOPC47A: MOUSE IGA
104) IGR*CL: MOUSE IGA
    102) MODSE IGA
103) MODSE IGA
104) IGE*CL: MOUSE IGE
105) IGE*CL': MOUSE IGE
106) IGE &*CL: MOUSE IGE
107) IGE BC*CL: MOUSE IGE
108) IGE MCMS*CL: MOUSE IGE
108) IGE MCMS*CL: MOUSE IGE MEMBRANE BOUND
121 IR-731: RAT IGD
122 IR-731: RAT IGG2
123 RAT IGG22*CL: RAT IGG26
124 RAT IGG26*CL: RAT IGG26
125 RAT IGG26*CL: RAT IGG26
126 RAT IGG26*CL: RAT IGG26
127 RAT IGG26*CL: RAT IGG26
128 RAT IGG26*CL: RAT IGG26
129 IR2*CL: RAT IGG
      1:5) MAT AGZID-CL: RAT IGGZD

1:6) RAT IGGZD-CL: RAT IGE

1:9) RZ-CL: RABBIT MU CHAIN SECRETED (ALLOTYPE A2)

1:1) PKJ-CL: RABBIT IGG

1:2) RABBIT IGG: RABBIT IGG

1:4) PCAMPASI-12-14-CL: RABBIT IGG

1:5) RABIGG: RABBIT IGG

1:6) RABIGG: CL: RABBIT IGG

1:7) P2A2-CL: RABBIT IGG

1:7) P3A2-CL: RABBIT IGG

1:7) P3A2-CL: RABBIT IGG

1:8) 39-LA, 20B -CL: RABBIT IGG

1:9) P3A5-CL: RABBIT IGG SUBCLASS

1:10) CT-12: COTIONTAIL RABBIT (SYLVILAGUS FLORIDANUS) IGG

1:1) PIKA: PIKA (OCHOTONA RUFENSIS) IGG
     130 CT-12: COTTONTAIL RABBIT (STYVILAGUS FLORIDANUS) IGG
131) PIKA: PIKA (OCHOTONA RUFENSIS) IGG
132) BA-3: HARE (LEPUS CALIFORNICUS) IGG
133] BA-11: HARE (LEPUS CALIFORNICUS) IGG
134) BA-1: HARE (LEPUS CALIFORNICUS) IGG
135) BA-5: HARE (LEPUS CALIFORNICUS) IGG
136) BA-1T: EUROPEAN HARE (LEPUF TIMIDUS) IGG
137) SYNIAM EAMSTER IGM'CL: SYRIAM HAMSTER LSH INBRED STRAIN
138) GPIGG1: GUINEA PIG IGG1
139) GP'IGG1: GUINEA PIG IGG1
140) GDIGG2: GUINEA PIG IGG2
     140) GPIGGE: GUINEA PIG IGG

141) MOO: DOG IGM

143) SREEP PSBC*CL: IGG1

144) BORSE IGG: HORSE IGG

145) BOVINE IGG: BOVINE IGG
      146) GOAT IGG: GOAT IGG
     146) GOAT IGG: GOAT IGG

147) CHICKEN IGM'CL: CHICKEN IGM

149 Racb'CL: ADULT Raja erinacea (LITTLE SKATE)

150) Ra20'CL: ADULT Raja erinacea (LITTLE SKATE)

151) Xanopus laevis IGM'CL: Xenopus laevis IGM

152) Xanopus laevis c8(II)'CL: Xenopus laevis IGM

153) Xanopus laevis c14(II)'CL: Xenopus laevis IGM

154) Xanopus laevis c35'CL: Xenopus laevis IGM
      154) Xenopus lasvis c35'CL: Xenopus lasvis IGM
155) Xenopus lasvis c40(II)'CL: Xenopus lasvis IGM
     156) Xenopus laevia JZ(I)'CL: Xenopus laevis IGM
157) Xenopus laevis J4(III)'CL: Xenopus laevis IGM
                     Xenopus laevis J6(I)'CL: Xenopus laevis IGM
     159) Xenopus laevis J12(IV)'CL: Xenopus laevis IGM
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GENERAL NOTES: HEAVY CONSTANT CHAINS

THE CHI, HINGE, CH2, CH3 AND CH4 DOMAINS ARE TABULATED TO CONFORM TO THEIR CODING NUCLECTIDE SEQUENCES RELATIVE TO THE PROPERTY OF THE CONFORM SEQUENCES ESTABLISHED BY SAKANO, H. ROGER, J. H., HUPPI, K., BRACK, C., TRAUNECKER, A., MALIE, THALL FROM THE TONE COMMANDED THE CONFORM SEQUENTIAL SECOND THE CONFORM SEQUENTIAL SECOND THE CONFORM SECOND THE CONFORM SECOND THE SEQUENTIAL SECOND THE CONFORM SECOND THE SEQUENTIAL SECOND THE SECOND

DISULFIDE BONDS ARE LOCATED AT THE FOLLOWING POSITIONS IF CYS IS PRESENT:

INTRACHAIN: 142-208,274-340,249-312,390-456,524-587.

HL-INTERCHAIN: 127 OR 128,198 OR 225,230,235.

HH-INTERCHAIN: 232,233,237,238,239,240,241A,G,M,P,V,8B,EE,KK,QQ,242,248,261,314.

INTERSUBUNIT: 328,444.

TO J-CHAIN: 495,627.

IDENTIFICATIONS OF SOME OF THESE DISULFIDE BONDS ARE NOT ABSOLUTELY CERTAIN.

THERE WOULD APPEAR TO BE POLYMORPHISM AMONG GAL, OU, SCO AND BOT/CO MU-CHAINS AS FOLLOWS:

GAL SER-334, VAL-358

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SPECIFIC NOTES: HEAVY CONSTANT CHAINS
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:) HUNGAN IGN'CL: THE AMINO ACID SEQUENCE WAS OBTAINED BY TRANSLATING A CLONE OF HUMAN FETAL LIVER DNA.
                5) BOT: FROM A CASE OF IGM HEAVY CHAIN DISEASE. THE AMINO ACID RESIDUES AT POSITIONS 451 TO 476, 519 TO 544 AND
608 TO 628 ARE IDENTICAL TO THAT OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN DNA
CONTAINING THE IGM GENE (TAKHABSHI, N. NAKAI, S. 6 HONJO, T. (1980) NUCL. ACIDS RES., 8, 5983-5991).
7) GLI: IT HAS NO VARIABLE REGION, AND WAS FROM A CASE OF HEAVY CHAIN DISEASE.
                                                      THE SEQUENCES OF MAH AND NIG-65 ARE IDENTICAL FOR POSITIONS 241 PP TO 485 WHERE BOTH SEQUENCES ARE DETERMINED. FOR MAH, THERE ARE FOUR OR FIVE N-ACETYL-D-GALACTOSAMINE OLIGOSACCHARIDES ATTACHED TO SER AT POSITIONS 241 AND ATTACHED TO SER ATTACHED TO SER AT POSITIONS 241 AND ATTACHED TO SER ATTACHED TO SER ATTACHED TO SER ATTACHED TO SER AT POSITION 241 AND THE ATTACHED TO SER ATTACHED TO ASN AT POSITIONS 241 P FOR NIG-65 THERE ARE THREE N-ACETYL-D-GALACTOSAMINE OLIGOSACCHARIDES ATTACHED TO SER AT N-ACETYL-D-GUCOSAMINE OLIGOSACCHARIDES ATTACHED TO ASN AT POSITIONS 314, 414 AND 465.
              9) WAR:
           10) MIG-65:
          11) ERI: THERE ARE THREE AMINO ACID RESIDUES BETWEEN POSITION 140 AND POSITION 142; THEY ARE ALA, VAL AND ALA. THE AUTHOR HAS RECENTLY INDICATED THAT THERE IS ONLY ONE AMINO ACID RESIDUE THERE AND IT IS ALA.
          14) HUMAN IGG3'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF THREE CLONES OF HUMAN GENOMIC DNA. THERE ARE FOUR EXONS: POSITIONS 216 TO 241B, 241C TO 241Q, 241R TO 241F, AND 241GG TO 243.

15) CMM'CL: THE AMINO ACID SEQUENCE IS GBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN CELL LINE CDNA. FROM A CASE OF HEAVY CHAIN DISEASE.
                                                    THE SEQUENCES OF HER, FRO AND JON ARE IDENTICAL.
THE SEQUENCES OF HER, FRO AND JON ARE IDENTICAL.
THE SEQUENCES OF HER, FRO AND JON ARE IDENTICAL.
            17) FRO:
                                                   FROM A CASE OF HEAVY CHAIN DISEASE.
FROM A CASE OF HEAVY CHAIN DISEASE.
FROM A CASE OF HEAVY CHAIN DISEASE.
           19) WIS:
         20) SPA:
21) ZOC:
                                                     OBTAINED FROM THE SAME PATIENT AS ZUC, AND EXISTED IN A MONOMER FORM.
                                                    THE SEQUENCES OF KUP AND BRU ARE IDENTICAL. THE SEQUENCES OF KUP AND BRU ARE IDENTICAL.
          231 KUP:
         26) CHA:
                                                  IT HAS NO VARIABLE REGION AND NO CH1 REGION, AND WAS FROM A CASE OF HEAVY CHAIN DISEASE. AMINO ACID RESIDUES FOUND AT POSITION 224 ARE THR AND SER.
        29) MIE: IN EARLIER EDITIONS, THE AMINO ACID RESIDUES AT POSITIONS 238, 285, 300 AND 331 LISTED BY US WERE INCORRECT.
301 CRA: FROM A CASE OF HEAVY CHAIN DISEASE.
        31) VAU: FROM A CASE OF HEAVY CHAIN DISEASE.
32) LEB: FROM A CASE OF HEAVY CHAIN DISEASE.
          33) EST:
                                                     IT HAS NO VARIABLE REGION AND NO CHI REGION, AND WAS FROM A CASE OF HEAVY CHAIN DISEASE.
                                                    THE GLY AT POSITION 462 IN IGG1 CHAIN IS CONSIDERED TO BE ASSOCIATED WITH THE DM(2) ALLOTYPE (COOK, E. & STEINBERG, A.G. (1979) MOL.IMMUNOL., 16,555-558).
       A.G. (1979) MOLTIMOUNDI, 16,555-58).

36) HUMAN IGGI'CL: THE AMINO ACID SEQUENCE IS CONTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A HUMAN FEAL LIVER DNA.

41) BUR: THE AMINO ACID RESIDUES AT POSITIONS 262,263,269,304,310,333,430,431,447,461 AND 490 HAVE RECENTLY BEEN REVISED
BY THE AUTHORS (PUTNAM,F.W., LIU,Y.S.V. & LOWIT.L.K. (1979), 1810L.CREM, 254,2865-2874,) FROM GLN, ASP, GLU, GLN, ASP,
ASN, GLN, GLY, ASP, GLU AND GLU TO GLX, ASX, GLX, GLX, ASX, GLX, ASX, GLX, AND GLN RESPECTIVELY.

43) CAR: THE SEQUENCE MAS OBTAINED AFTER DIGESTION WITH PROTEASES. PROTEASES FROM S. SANGUIS AND S. PNEUMONIAE CLEAVED
BETWEEN POSITIONS 141C AND 241D, AND THAT FROM H. INFLUENZEE BETWEEN POSITIONS 241G AND 241H.

47) HUMAN IGG: CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN FETAL
LIVER DNA. THIS GENE IS NOT EXPRESSED DUE TO THE LACK OF A SWITCH REGION, AND IS THUS DESIGNATED AS

48) HUMAN IGG2' CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC

DNA. THE MAINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC

51) HUMAN IGG2' CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC

52) HUMAN IGG2' CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC

53) HUMAN IGG2' CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC

54) HUMAN IGG2' CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC
          53) HUMAN IGCA'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF HUMAN GENOMIC
      DNA.

55) HUMAN IGE*CL: THE AMINO ACID SECUENCE IS OBTAINED BY TRANSLATING THE NUCLECTIDE SEQUENCES OF CLONES OF HUMAN GENOMIC DNA FROM FETAL LIVER (NISHIDA,Y. MIRIT: HISAJIMA, H. & HONJO.T. (1982) FROC.NAT.ACAD.SCT.USA,79,3833-3837) AND PLACENTA WAX.E.E. BATTEY.J. XEYS. XERSCH, IR. & TEDER,P. (1982) ENDO.NAT.ACAD.SCT.USA,79,3833-3837) AND PLACENTA WAX.E.E. BATTEY.J. XEYS. XEYS. THE JEDER,P. (1982) ENDO.NAT.ACAD.SCT.USA,79,3833-3837) AND PLACENTA LIVER.SCT.USA,79,3833-3837) AND PLACENTA LIVER.SCT.USA,79,3833-3837 AND PLACENTA LIVER.
                                                           THE AMINO ACID SEQUENCE IS COTAINED BY TRANSLATING THE NUCLECTICE SEQUENCE OF A CLONE OF HUMAN CDNA.
THE LENGTHS OF INTERVENING SEQUENCES BETWEEN CH: AND CH2 AND CH3 AND CH3 AND CH4 ARE 110 279 AND 107
BASE-PAIRS RESPECTIVELY. MATTHYSESHS, 3: RABBITTS, TH. (1980) NUCL. ACIDS RES. 3, 703-713; HAVE ALSO OBTAINED
AMINO ACID RESIDUES 583 TO 628 FROM THE NUCLECTICE SEQUENCES. CALAME, N. ROGERS. 1, 203-713; HAVE ALSO OBTAINED
AMINO ACID RESIDUES 583 TO 628 FROM THE NUCLECTICE SEQUENCES. CALAME, N. ROGERS. 1, 203-714; M. 174-NT, D.
WALL R. & HOOD, 1 (1980) NATURE 284, 52-55) BY NUCLECTICE SEQUENCING OF AMINO ACIDS 320 TO 343 AND 593 TO 628
FOUND ACT CODING FOR THE AT FOSITION 328.
      FOUND ACT CODING FOR THE AT POSITION 328.

67) IGM'CL': THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA. A SINGLE AMINO ACTO SUSPITION TO POSITION 436 FROM SER TO ASN RESULTS IN A MUTANT PROTEIN MICH IS DEFECTIVE IN PROTEIN ALL ACAD SCIUSA, 83, 7678-7682;

69) MUTANT 102 CL: IT LACKS CODONS 601 TO 614, SC THAT PREDOMINANTLY MONOMERIC IGM WAS PRODUCED BY THIS CELL LINE.

10) MOPCIO 42 MEMBER CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CONA CLONE.

11) MOPCIO 54 CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CONA CLONE.

12) IGD'CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA.

13) IGD SECR'CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.

14) IGD SECR'CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.

15) IGD SECR'CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.

16) IGD SECR'CL: THE AMINO ACTO SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.
       TO IGD MEMBERCE: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE GENOMIC DNA.
     F1) IGG1 CL: THE AMINO ACID SEQUENCE IS STRAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF NEWBORN MOUSE DHA
THE INCOME SEQUENCE BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF NEWBORN MOUSE DHA
BASE PARTS RESPONSITE THE NATIONAL SEQUENCE BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CINA.

F2) IGG1 MODGS CL: THE AMINO ACID SEQUENCE IS COTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CINA.
      34) IF2'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA FROM CELL LINE 172. THE CHI REGION IS DELETED.
      50' IGG28 (A) CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A TIONE OF MOUSE DNA. THE ENGTHS OF INTERVENING SEQUENCES BETWEEN THIS AND HINGE, HINGE AND CH2, AND CH2 AND CH3 ARE 316, 108, AND 112 AND 112 AND THE MOUSE DNA.
      STY IGG28 (A) CLL: THE AMING ACID SEQUENCE IS COTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA.

THE LENGTHS IF INTERVENING SEQUENCES BETWEEN CHI AND HINGE, HINGE AND CHZ, AND CHZ AND
     F3) IGG28 (B) (CL: THE AMING ACID SEQUENCE IS CBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE ONA. THE ENGTHS OF INTERVENING SEQUENCES BETWEEN CHI AND HINGE, HINGE AND CH2 AND CH2 AND CH3 ARE 317, 108, AND 113 BASE-FAIRS RESPECTIVELY.

19) IGG28 MEDG9 (CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.

10) MGC11: THE AMING ACID RESIDUES AT POSITION 363 WERE FOUND TO BE ILE AND LEU.
       10 10.1: This protein is obtained from a mutant of MPC11 with a Deletion of 99 Mucleotides including the 3' end of the CH1 ERON, JOVING RISE TO A DELETION OF THE ENTIRE CH1 REGION OF THE PROTEIN.
      -2) IGG2A(A) CL: THE AMING ACID SEQUENCE IS COTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.
-3) 17/9 CL: THE FAT FRAGMENT OF 17/9 (IGG2A-KAPPA) HAS BEEN CRYSTALLIZED.
      44) IGG2A(B) CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLECTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.
44) IGG2A MEDG*CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLECTIDE SEQUENCE OF A CLONE OF MOUSE CDNA.
   140 IGA/CL: THE AMING ACID SECURNCE IS GETAINED BY TRANSLATING THE NUCLEOTIDE SECUENCE OF A CLONE OF MOUSE CDMA.
110 IGA/CL: THE AMING ACID SECUENCE IS GETAINED BY TRANSLATING THE NUCLEOTIDE SECUENCE OF A CLONE OF BALB/C MOUSE LIVER
120 IT THE COLOR SEMENT IN THE HE HAD REGION IS NOT ON A SEPRANTE EXON. THE FIRST THREE AMING ACID RESIDES
121 IT THE COLOR OF THE COLOR
MOPC511: CARBCHYTRATES ARE ATTACHED AT POSITIONS 154 AND 483.

174) IGE CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF MOUSE DNA FROM AN IGE-FRODUCING HYBRICOMA.
IGE-PRODUCING HYBRICOMA.

10- IGE a'CL: FROM BALB-1 MOUSE LIVER DNA.

10- IGE b'CL: FROM BILLA MOUSE LIVER TNA.

10- IGE MODE: CL: THOM MOUSE LIVER TNA.

10- IGE MODE: CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF DNA FROM NEWBORN MOUSE.
NOTES.

1.1 RAT IGO'CL: THE AMING ACID SEQUENCE WAS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RAT CDNA.

1.2 IR2'CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RAT CDNA.

1.3 IR-162'CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RAT CNA.

1.4 PGAMBAB1-12.14'CL: THE AMING ACID SEQUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RABBIT CNA.
... RABIGG: THE AMING ACID SEQUENCE FOR POSITIONS 266 TO 275 AND 321 TO 336 WAS ALSO CONFIRMED BY OTHERS (TEHERANI,J., DAFRA,J.C., AJJARWAL,S. 4 MANDY,W.J. (1979) EUR.J.IMMUNOL.,9,690-695.).
22 P2A2 CL: THE AMING ACTS SECUENCE IS OBTAINED BY TRANSLATING THE NUCLEOTIDE SEQUENCE OF A CLONE OF RABBIT COMA.
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SPECIFIC NOTES: HEAVY CONS

143) SHEEP PSEC'CL: TRANSLATED 144) BORSE IGG: AS COMPARED WI 147) CRICKEN IGN'CL: THE AMING

148) Elope VE'CL: FROM Elops sa 152) Xenopus laevis c8(II)'CL:

153) Xenopus laevis c14(II)'CL:
- THE FOLLOWING WERE EQUALLY A

AT POSITION

SPECIFIC NOTES: HEAVY CONSTANT CHAINS (cont'd)

- 143) SHEEP PSHC'CL: TRANSLATED FROM CDNA OF SHEEP LYMPHOCYTES
- 143) SHEEF PSHC CE: TRANSLATED FROM COMA OF SHEEF LIMFHOCITES
 144) BORSE IGG: AS COMPARED WITH HORSE IGG, THE HORSE T PROTEIN HAD VAL AT POSITION 463, GLU AT 464, AND HIS AT 474.
 147) CHICKEN IGM'CL: THE AMINO ACID SEQUENCE IS OBTAINED BY TRANSLATING THE SEQUENCE OF A CLONE OF CHICKEN CDNA.
- 148) Elops VH'CL: FROM Elops saurus (LADYFISH).
- 152) Xenopus laevis c8(II)'CL: ALSO KNOWN AS XIg8'CL.
- 153) Xenopus laevis c14(II)'CL: ALSO KNOWN AS XIg14'CL.
- + THE FOLLOWING WERE EQUALLY AND MOST FREQUENTLY OCCURRING:

AT POSITION	RESIDUES
113D 113E	(ILE, GLN), (ILE, GLU)
1375	(CYS, SER) (THR, SER)
158	(LYS. ASN)
224	(ARG, GLU)
241B 243I	(PRO, CYS)
281	(ALA, SER)
307	(PRO,GLU) (PRO,LYS)
326	(PRO, THR)
343	(THR, ASN)
351A 403	(LEU, THR, ASN)
452	(THR, ASN) (ASP, ASN)
496C	(PRO, ALA)
511	(ARG, GLU)
511 532 545	(ALA, GLU)
รียี่ดีฮ	(PRO, LEU)
637	(MET, ASP) (LEU, VAL)
657	(GLU, GLN)
662 663	(ILE, VAL, ALA)
003	(ILE, SER)